

SEQUENCE LISTING

<110> Liang, Yanbin  
Woodward, David F.

<120> Human Prostaglandin FP Receptor Variants  
and Methods of Using Same

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<160> 40

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<212> DNA

<213> Homo sapeins

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His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys	
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Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly	
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Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val	
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Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu	
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Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Gly Tyr Arg Ile Ile Leu	
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 195 200 205  
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 210 215 220  
 Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
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Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe	
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tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc	144
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile	
35 40 45	
gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca	192
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala	
50 55 60	
tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc	240
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly	
65 70 75 80	
cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa	288
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys	
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gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt	336
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly	
100 105 110	
atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg	384
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115 120 125	
atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct	432
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser	
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acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc	480
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys	
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Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp	
165 170 175	
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Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp	
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Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly
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Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu			
	195	200	205
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly			
	210	215	220
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly			
	225	230	235
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys			
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Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe	
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tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc	144
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile	
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Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly	
65 70 75 80	
cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa	288
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys	

	85	90	95	
	gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt			336
	Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly			
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	atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg			384
	Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val			
	115	120	125	
	atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct			432
	Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser			
	130	135	140	
	acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc			480
	Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys			
	145	150	155	160
	ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac			528
	Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp			
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	Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp			
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	atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttt ctg			624
	Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu			
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	ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga			672
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	Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys			
	245	250	255	
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	Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Gly Tyr Arg Ile Ile Leu			
	260	265	270	
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Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
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Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp	
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Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp	
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Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu	
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ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga	672
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly	
210 215 220	
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Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly	
225 230 235 240	
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt	768
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys	
245 250 255	
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Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Val Lys Glu Thr His Leu	
260 265 270	
cag atg aga ctt tgg act tgg gac ttt cga gtt aat gct ttg gag gac	864
Gln Met Arg Leu Trp Thr Trp Asp Phe Arg Val Asn Ala Leu Glu Asp	
275 280 285	
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Tyr Cys Glu Gly Leu Thr Val Phe *	
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<213> Homo sapiens

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				165					170					175	
Tyr	Lys	Ile	Gln	Ala	Ser	Arg	Thr	Trp	Cys	Phe	Tyr	Asn	Thr	Glu	Asp
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Arg	Ser	His	His	Leu	Glu	Met	Val	Ile	Gln	Leu	Leu	Ala	Ile	Met	Cys
				245					250					255	
Val	Ser	Cys	Ile	Cys	Trp	Ser	Pro	Phe	Leu	Val	Lys	Glu	Thr	His	Leu
			260					265					270		
Gln	Met	Arg	Leu	Trp	Thr	Trp	Asp	Phe	Arg	Val	Asn	Ala	Leu	Glu	Asp
		275					280					285			
Tyr	Cys	Glu	Gly	Leu	Thr	Val	Phe								
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<210> 9

<211> 1221

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(804)

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1				5					10					15		
ctt	tca	aac	aca	acc	tgc	cag	acg	gaa	aac	cgg	ctt	tcc	gta	ttt	ttt	96
Leu	Ser	Asn	Thr	Thr	Cys	Gln	Thr	Glu	Asn	Arg	Leu	Ser	Val	Phe	Phe	
			20					25					30			
tca	gta	atc	ttc	atg	aca	gtg	gga	atc	ttg	tca	aac	agc	ctt	gcc	atc	144

Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile	
35 40 45	
gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca	192
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala	
50 55 60	
tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc	240
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly	
65 70 75 80	
cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa	288
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys	
85 90 95	
gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt	336
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly	
100 105 110	
atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta ggc agt gtg	384
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val	
115 120 125	
atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct	432
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser	
130 135 140	
acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc	480
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys	
145 150 155 160	
ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac	528
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp	
165 170 175	
tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac	576
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp	
180 185 190	
atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttt ctg	624
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu	
195 200 205	
ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga	672
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly	
210 215 220	
att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc	720
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly	
225 230 235 240	
aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt	768
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys	

245	250	255	
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Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Arg *			
260	265		

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ttatacatgg gtgctggctc agacgtgaca cctgaggctc cagaactgga agtttatgcc	934
gtcaagttac aatggccaac attggaataa atggaaatca ttctctggaa acctgtgaaa	994
caacactttt tgctctccga atggcaacat ggaatcaaat cttagatcct tgggtatata	1054
ttcttctacg aaaggctgtc cttaagaatc tctataagct tgccagtcaa tgctgtggag	1114
tgcattgtcat cagcttacat atttgggagc ttagttccat taaaaattcc ttaaagggtg	1174
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 <212> PRT  
 <213> Homo sapiens

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Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile	
35 40 45	
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala	
50 55 60	
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly	
65 70 75 80	
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys	
85 90 95	
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly	
100 105 110	
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val	
115 120 125	
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser	
130 135 140	
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys	
145 150 155 160	
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp	
165 170 175	
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp	
180 185 190	
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu	
195 200 205	
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly	
210 215 220	
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly	
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Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Arg	

260

265

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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(825)

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1 5 10 15  
  
ctt tca aac aca acc tgc cag acg gaa aac cgg ctt tcc gta ttt ttt 96  
Leu Ser Asn Thr Thr Cys Gln Thr Glu Asn Arg Leu Ser Val Phe Phe  
20 25 30  
  
tca gta atc ttc atg aca gtg gga atc ttg tca aac agc ctt gcc atc 144  
Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
35 40 45  
  
gcc att ctc atg aag gca tat cag aga ttt aga cag aag tcc aag gca 192  
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
  
tcg ttt ctg ctt ttg gcc agc ggc ctg gta atc act gat ttc ttt ggc 240  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
  
cat ctc atc aat gga gcc ata gca gta ttt gta tat gct tct gat aaa 288  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
  
gaa tgg atc cgc ttt gac caa tca aat gtc ctt tgc agt att ttt ggt 336  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
  
atc tgc atg gtg ttt tct ggt ctg tgc cca ctt ctt cta gcc agt gtg 384  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val  
115 120 125  
  
atg gcc att gag cgg tgt att gga gtc aca aaa cca ata ttt cat tct 432  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
  
acg aaa att aca tcc aaa cat gtg aaa atg atg tta agt ggt gtg tgc 480  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160

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ttg ttt gct gtt ttc ata gct ttg ctg ccc atc ctt gga cat cga gac 528
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp
      165              170              175

tat aaa att cag gcg tcg agg acc tgg tgt ttc tac aac aca gaa gac 576
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp
      180              185              190

atc aaa gac tgg gaa gat aga ttt tat ctt cta ctt ttt tct ttt ctg 624
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu
      195              200              205

ggg ctc tta gcc ctt ggt gtt tca ttg ttg tgc aat gca atc aca gga 672
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly
      210              215              220

att aca ctt tta aga gtt aaa ttt aaa agt cag cag cac aga caa ggc 720
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly
      225              230              235              240

aga tct cat cat ttg gaa atg gta atc cag ctc ctg gcg ata atg tgt 768
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys
      245              250              255

gtc tcc tgt att tgt tgg agc cca ttt ctg aca cat tgg ggt aaa gaa 816
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Thr His Trp Gly Lys Glu
      260              265              270

att cca tga tccctcctgt gcctaagcca cccagtgga cctggtcttc 865
Ile Pro *

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ttgcaccatc cctgtggctg gaggtttgag atactgacag cgataagaca ctcaacgaga 925
aatgacagaa aaacaagggtg tggatggaga ggcaacatga aagtggatca aacaacttat 985
acatgggtgc tggctcagac gtgacacctg aggtctccaga actggaagtt tatgccgtca 1045
agttacaatg gccaacattg gaataaatgg aaatcattct ctggaaacct gtgaaacaac 1105
acttttttgc ctccgaatgg caacatggaa tcaaatctta gatccttggg tatatatctt 1165
tctacgaaaag gctgtcctta agaatctcta taagcttgcc agtcaatgct gtggagtgc 1225
tgtcatcagc ttacatatatt gggagcttag ttccattaaa aattccttaa aggttgctgc 1285
tatttctgag tcaccagttg cagagaaatc agcaagcacc tag 1328

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 <212> PRT  
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 Ser Val Ile Phe Met Thr Val Gly Ile Leu Ser Asn Ser Leu Ala Ile  
 35 40 45

Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala  
50 55 60  
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly  
65 70 75 80  
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys  
85 90 95  
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly  
100 105 110  
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val  
115 120 125  
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser  
130 135 140  
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys  
145 150 155 160  
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp  
165 170 175  
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp  
180 185 190  
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu  
195 200 205  
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly  
210 215 220  
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly  
225 230 235 240  
Arg Ser His His Leu Glu Met Val Ile Gln Leu Leu Ala Ile Met Cys  
245 250 255  
Val Ser Cys Ile Cys Trp Ser Pro Phe Leu Thr His Trp Gly Lys Glu  
260 265 270  
Ile Pro

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<212> DNA  
<213> Homo sapiens

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<222> (152)...(1228)

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acttgagtgg ttggctttta tctccacaac a atg tcc atg aac aat tcc aaa 172  
Met Ser Met Asn Asn Ser Lys

1 5

cag cta gtg tct cct gca gct gcg ctt ctt tca aac aca acc tgc cag 220  
Gln Leu Val Ser Pro Ala Ala Ala Leu Leu Ser Asn Thr Thr Cys Gln  
10 15 20

acg gaa aac cgg ctt tcc gta ttt ttt tca gta atc ttc atg aca gtg 268



Thr	Glu	Asn	Arg	Leu	Ser	Val	Phe	Phe	Ser	Val	Ile	Phe	Met	Thr	Val		
	25					30					35						
gga	atc	ttg	tca	aac	agc	ctt	gcc	atc	gcc	att	ctc	atg	aag	gca	tat	316	
Gly	Ile	Leu	Ser	Asn	Ser	Leu	Ala	Ile	Ala	Ile	Leu	Met	Lys	Ala	Tyr		
	40				45					50					55		
cag	aga	ttt	aga	cag	aag	tcc	aag	gca	tcg	ttt	ctg	ctt	ttg	gcc	agc	364	
Gln	Arg	Phe	Arg	Gln	Lys	Ser	Lys	Ala	Ser	Phe	Leu	Leu	Leu	Ala	Ser		
				60				65						70			
ggc	ctg	gta	atc	act	gat	ttc	ttt	ggc	cat	ctc	atc	aat	gga	gcc	ata	412	
Gly	Leu	Val	Ile	Thr	Asp	Phe	Phe	Gly	His	Leu	Ile	Asn	Gly	Ala	Ile		
			75					80					85				
gca	gta	ttt	gta	tat	gct	tct	gat	aaa	gaa	tgg	atc	cgc	ttt	gac	caa	460	
Ala	Val	Phe	Val	Tyr	Ala	Ser	Asp	Lys	Glu	Trp	Ile	Arg	Phe	Asp	Gln		
		90					95					100					
tca	aat	gtc	ctt	tgc	agt	att	ttt	ggc	atc	tgc	atg	gtg	ttt	tct	ggc	508	
Ser	Asn	Val	Leu	Cys	Ser	Ile	Phe	Gly	Ile	Cys	Met	Val	Phe	Ser	Gly		
	105					110					115						
ctg	tgc	cca	ctt	ctt	cta	ggc	agt	gtg	atg	gcc	att	gag	cgg	tgt	att	556	
Leu	Cys	Pro	Leu	Leu	Leu	Gly	Ser	Val	Met	Ala	Ile	Glu	Arg	Cys	Ile		
	120				125					130					135		
gga	gtc	aca	aaa	cca	ata	ttt	cat	tct	acg	aaa	att	aca	tcc	aaa	cat	604	
Gly	Val	Thr	Lys	Pro	Ile	Phe	His	Ser	Thr	Lys	Ile	Thr	Ser	Lys	His		
				140					145					150			
gtg	aaa	atg	atg	tta	agt	ggc	gtg	tgc	ttg	ttt	gct	gtt	ttc	ata	gct	652	
Val	Lys	Met	Met	Leu	Ser	Gly	Val	Cys	Leu	Phe	Ala	Val	Phe	Ile	Ala		
			155					160					165				
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Leu	Leu	Pro	Ile	Leu	Gly	His	Arg	Asp	Tyr	Lys	Ile	Gln	Ala	Ser	Arg		
		170					175					180					
acc	tgg	tgt	ttc	tac	aac	aca	gaa	gac	atc	aaa	gac	tgg	gaa	gat	aga	748	
Thr	Trp	Cys	Phe	Tyr	Asn	Thr	Glu	Asp	Ile	Lys	Asp	Trp	Glu	Asp	Arg		
	185					190					195						
ttt	tat	ctt	cta	ctt	ttt	tct	ttt	ctg	ggg	ctc	tta	gcc	ctt	ggc	gtt	796	
Phe	Tyr	Leu	Leu	Leu	Phe	Ser	Phe	Leu	Gly	Leu	Leu	Ala	Leu	Gly	Val		
	200				205					210					215		
tca	ttg	ttg	tgc	aat	gca	atc	aca	gga	att	aca	ctt	tta	aga	gtt	aaa	844	
Ser	Leu	Leu	Cys	Asn	Ala	Ile	Thr	Gly	Ile	Thr	Leu	Leu	Arg	Val	Lys		
				220				225						230			
ttt	aaa	agt	cag	cag	cac	aga	caa	ggc	aga	tct	cat	cat	ttg	gaa	atg	892	
Phe	Lys	Ser	Gln	Gln	His	Arg	Gln	Gly	Arg	Ser	His	His	Leu	Glu	Met		

235	240	245	
gta atc cag ctc ctg gcg ata atg tgt gtc tcc tgt att tgt tgg agc			940
Val Ile Gln Leu Leu Ala Ile Met Cys Val Ser Cys Ile Cys Trp Ser			
250	255	260	
cca ttt ctg gtt aca atg gcc aac att gga ata aat gga aat cat tct			988
Pro Phe Leu Val Thr Met Ala Asn Ile Gly Ile Asn Gly Asn His Ser			
265	270	275	
ctg gaa acc tgt gaa aca aca ctt ttt gct ctc cga atg gca aca tgg			1036
Leu Glu Thr Cys Glu Thr Thr Leu Phe Ala Leu Arg Met Ala Thr Trp			
280	285	290	295
aat caa atc tta gat cct tgg gta tat att ctt cta cga aag gct gtc			1084
Asn Gln Ile Leu Asp Pro Trp Val Tyr Ile Leu Leu Arg Lys Ala Val			
300	305	310	
ctt aag aat ctc tat aag ctt gcc agt caa tgc tgt gga gtg cat gtc			1132
Leu Lys Asn Leu Tyr Lys Leu Ala Ser Gln Cys Cys Gly Val His Val			
315	320	325	
atc agc tta cat att tgg gag ctt agt tcc att aaa aat tcc tta aag			1180
Ile Ser Leu His Ile Trp Glu Leu Ser Ser Ile Lys Asn Ser Leu Lys			
330	335	340	
gtt gct gct att tot gag tca cca gtt gca gag aaa tca gca agc acc			1228
Val Ala Ala Ile Ser Glu Ser Pro Val Ala Glu Lys Ser Ala Ser Thr			
345	350	355	
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gatgggcaac tagaattaca gcagtttcaa actctacccat ggataatgca aacaaaccga			2068
agctacatgc caatgatagg tgcaaagaat attggcaaaa ggtgctttac cttgagccat			2128
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tgtaattcaa ccaaaagaat ttcaataccc attcaaattg tcctaggtct atcagaaatt			2488
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tcattaaaaa tgggattcat ttaaaaatta atctttccct gttaggctga tttcagattc			2608

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gaatttatatt catacagtta ctttaagagt ttgatgtctt gtgaacagag atataaggaa 2728
ccattctcca tcttctctta tcatgctggg tacaatgctt ctatgaatat ttccatgtat 2788
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<211> 359
<212> PRT
<213> Homo sapiens
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35 40 45
Ala Ile Leu Met Lys Ala Tyr Gln Arg Phe Arg Gln Lys Ser Lys Ala
50 55 60
Ser Phe Leu Leu Leu Ala Ser Gly Leu Val Ile Thr Asp Phe Phe Gly
65 70 75 80
His Leu Ile Asn Gly Ala Ile Ala Val Phe Val Tyr Ala Ser Asp Lys
85 90 95
Glu Trp Ile Arg Phe Asp Gln Ser Asn Val Leu Cys Ser Ile Phe Gly
100 105 110
Ile Cys Met Val Phe Ser Gly Leu Cys Pro Leu Leu Leu Gly Ser Val
115 120 125
Met Ala Ile Glu Arg Cys Ile Gly Val Thr Lys Pro Ile Phe His Ser
130 135 140
Thr Lys Ile Thr Ser Lys His Val Lys Met Met Leu Ser Gly Val Cys
145 150 155 160
Leu Phe Ala Val Phe Ile Ala Leu Leu Pro Ile Leu Gly His Arg Asp
165 170 175
Tyr Lys Ile Gln Ala Ser Arg Thr Trp Cys Phe Tyr Asn Thr Glu Asp
180 185 190
Ile Lys Asp Trp Glu Asp Arg Phe Tyr Leu Leu Leu Phe Ser Phe Leu
195 200 205
Gly Leu Leu Ala Leu Gly Val Ser Leu Leu Cys Asn Ala Ile Thr Gly
210 215 220
Ile Thr Leu Leu Arg Val Lys Phe Lys Ser Gln Gln His Arg Gln Gly
225 230 235 240
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